

FORM PTO-1449 U.S. Department of Commerce Patent and Trademark Office List of Documents Cited by Applicant		Attorney Docket No. 431734/2 <div style="text-align: center;"> RECEIVED SEP 06 2002 TECH CENTER 1600/2900 </div>		Serial No. 09/998,058			
		Applicant(s): David W. Threadgill and Robert W. Williams					
		Filing Date: November 30, 2001		Group 1645			
U.S. PATENT DOCUMENTS							
Examiner Initial		Document Number	Date	Name	Class	Subclass	Filing date if Appropriate
FOREIGN PATENT DOCUMENTS							
		Document Number	Date	Country	Name of Patentee or Applicant		Translation Yes No
OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)							
48	1.	WELLS et al., <i>Genomics meets genetics: towards a mutant map of the mouse, Mammalian Genome</i> 11 :472-477 (2000). ✓					
48	2.	DARVASI, <i>Experimental strategies for the genetic dissection of complex traits in animal models, Nature Genetics</i> 18 :19-24 (January 1998). ✓					
	3.	KLYSIK et al., <i>An Integrated Gene and SSLP BAC Map Framework of Mouse Chromosome 11, Genomics</i> 62 :123-128 (1999). ✓					
	4.	THREADGILL et al., <i>SSLPs to map genetic differences between the 129 inbred strains and closed-colony, random-bred CD-1 mice, Mammalian Genome</i> 8 :441-442 (1997).					
	5.	SCHALKWYK et al., <i>Panel of Microsatellite Markers for Whole-Genome Scans and Radiation Hybrid Mapping and a Mouse Family Tree, Genome Research</i> 8 :878-887 (1999).					
	6.	SCHRIML et al., <i>Use of Denaturing HPLC to Map Human and Murine Genes and to Validate Single-Nucleotide Polymorphisms, BioTechniques</i> 28 , No. 4:740-744 (2000).					
48	7.	AKIYOSHI et al., <i>A genetic linkage map of the MSM Japanese wild mouse strain with restriction landmark genomic scanning (RLGS), Mammalian Genome</i> 11 :356-359 (2000).					

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8.	VAN ETTEN et al., <i>Radiation hybrid map of the mouse genome</i> , <u>Nature Genetics</u> 22 :384-387 (1999).		
9.	LINDBLAD-TOH et al., <i>Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse</i> , <u>Nature Genetics</u> 24 :381-386 (2000).		
10.	NADEAU et al., <i>Analysing complex genetic traits with chromosome substitution strains</i> , <u>Nature Genetics</u> 24 :221-225 (2000).		
11.	DARVASI, <i>Interval-specific congenic strains (ISCS): an experimental design for mapping a QTL into a 1-centimorgan interval</i> , <u>Mammalian Genome</u> 8 :163-167 (1997).		
12.	LANDER et al., <i>Mapping Mendelian Factors Underlying Quantitative Traits Using RFLP Linkage Maps</i> , <u>Genetics</u> 121 :185-199 (January 1989).		
13.	RAO, <i>Genetic Dissection of Complex Traits: An Overview</i> , <u>Advances in Genetics</u> 42 :13-34 (2001).		
14.	THREADGILL et al., <i>Genealogy of the 129 inbred strains: 129/SvJ is a contaminated inbred strain</i> , <u>Mammalian Genome</u> 8 :390-393 (1997).		
15.	MOTT et al., <i>A method for fine mapping quantitative trait loci in outbred animal stocks</i> , <u>PNAS</u> 97 , No. 23:12649-12654 (November 7, 2000).		
16.	AMOS et al., <i>Cost of Linkage versus Association Methods</i> , <u>Advances in Genetics</u> 42 :213-221 (2001).		
17.	SCHORK, <i>Genome Partitioning and Whole-Genome Analysis</i> , <u>Advances in Genetics</u> 42 :299-322 (2001).		
18.	GOLDGAR, <i>Major Strengths and Weaknesses of Model-free Methods</i> , <u>Advances in Genetics</u> 42 :241-251 (2001).		
19.	BLANGERO et al., <i>Variance Component Methods for Detecting Complex Trait Loci</i> , <u>Advances in Genetics</u> 42 :151-181 (2001).		

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*Examiner Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

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